

This listing of claims replaces all prior versions, and listings, of claims in the application.

Listing of CLAIMS:

1. (Currently Amended) A method for sequencing a terminal portion of an oligomer, comprising:

(a) contacting said oligomer with a **mass defect** labeling moiety to covalently attach a label to the terminus of the oligomer and form a labeled oligomer, said labeling moiety comprising at least one element having an atomic number from 17 to 77, with the proviso that said element is other than sulfur or phosphorus;

(b) fragmenting said labeled oligomer using an enzymatic, chemolytic or mass spectrometric fragmentation method to produce labeled oligomer fragments; and

(c) ~~analyzing said labeled oligomer fragments using a mass spectrometric fragmentation method to determine~~ **determining** the sequence of at least two terminal residues **of said labeled oligomer, said sequence determination step comprising identifying a mass spectrum data corresponding to said labeled oligomer fragment or a mass spectrum fragment thereof, wherein said identification step is based at least in part on the mass defect of at least a portion of said labeling moiety.**

2. (Original) The method of claim 1, wherein said labeling moiety comprises at least one element of atomic number 35 to 63.

3. (Original) The method of claim 2, wherein said labeling moiety comprises at least one element of atomic number 39 to 58.

4. (Original) The method of claim 2, wherein said labeling moiety comprises at least one element selected from the group consisting of bromine, iodine, europium and yttrium.

5. (Original) The method of claim 4, wherein said element is europium.
6. (Original) The method of claim 4, wherein said element is yttrium.
7. (Original) The method of claim 4, wherein said element is bromine.
8. (Original) The method of claim 4, wherein said element is iodine.
9. (Original) The method of claim 1, wherein said oligomer is selected from the group consisting of a protein, an oligonucleotide, an oligosaccharide and a lipid.
10. (Original) The method of claim 9, wherein said oligomer is an oligonucleotide.
11. (Original) The method of claim 9, wherein said sequence is at least three residues.
12. (Original) The method of claim 9, wherein said sequence is at least four residues.
13. (Original) The method of claim 1, wherein several oligomers, each labeled with a different number of mass defect elements are mixed prior to said fragmenting or analyzing step.
14. (Currently Amended) A method for sequencing a portion of an oligomer in an oligomer mixture, said method comprising:
 - (a) contacting said oligomer mixture with a terminus labeling moiety to covalently attach a label to the terminus of said oligomer and form a labeled oligomer

mixture, said terminus labeling moiety comprising at least one element having an atomic number from 17 to 77, with the proviso that said element is other than sulfur or phosphorus;

(b) separating individual labeled oligomers in said labeled oligomer mixture; and

(c) analyzing said individual labeled oligomers from step (b) by a mass spectrometric method to determine the sequence of at least two terminus residues, **said analysis step comprising identifying a mass spectrum data corresponding to said labeled oligomer or a mass spectrum fragment thereof, wherein said identification step is based at least in part on the mass defect of at least a portion of said labeling moiety.**

15. (Original) A method in accordance with claim 14, wherein said element has an atomic number of from 35 to 63.

16. (Original) A method in accordance with claim 14, wherein said element has an atomic number of from 39 to 58.

17. (Original) A method in accordance with claim 14, wherein said element is selected from the group consisting of bromine, iodine, europium and yttrium.

18. (Original) A method in accordance with claim 14, further comprising a step prior to step (a) of isolating a group of oligomers from a biological sample.

19. (Original) A method in accordance with claim 18, wherein said biological sample is from a diseased tissue sample.

20. (Original) A method in accordance with claim 18, wherein said biological sample is from a healthy tissue sample.

21. (Original) A method in accordance with claim 14, wherein said separating is conducted by at least one method of capillary electrophoresis of the labeled oligomer mixture.

22. (Original) A method in accordance with claim 14, wherein said mass spectrometric method uses ESI-TOF MS.

23. (Currently Amended) A method for structure and function analysis of an oligomer having a plurality of residues, said method comprising:

(a) contacting said oligomer with a mass defect labeling reagent to differentially label exposed residues and unexposed residues and produce a differentially labeled oligomer **comprising a mass defect labeling moiety**, wherein said mass defect labeling reagent comprises at least one element having an atomic number of from 17 to 77 that is other than sulfur or phosphorus;

(b) analyzing said differentially labeled oligomer by a mass spectrometric method to determine sequences of said oligomer that are exposed in the three-dimensional structure and sequences of said oligomer that are unexposed in the three-dimensional structure, **said analysis step comprising identifying a mass spectrum data corresponding to said labeled oligomer or a mass spectrum fragment thereof, wherein said identification step is based at least in part on the mass defect of at least a portion of said labeling moiety.**

24. (Original) A method in accordance with claim 23, wherein said oligomer is a protein, a nucleic acid, or an oligosaccharide.

25. (Original) A method in accordance with claim 23, wherein said mass defect labeling reagent comprises at least one element of atomic number 35 to 63.

26. (Original) A method in accordance with claim 26, wherein said mass defect labeling reagent is bromine and said oligomer is a protein.

27. (Original) A method in accordance with claim 23, wherein said mass defect labeling reagent comprises at least one element of atomic number 39 to 58.

28. (Original) A method in accordance with claim 23, wherein said differentially labeled oligomer is fragmented by enzymatic or chemolytic methods prior to step (b).

29. (Original) A method in accordance with claim 23, wherein said oligomer is a protein, said mass defect is bromine or iodine and said exposed residues comprises a portion of the tyrosine residues present in said protein.

30. (Original) A method in accordance with claim 23, wherein said mass spectrometric method uses ESI-TOF MS.

31. (Original) A method in accordance with claim 29, wherein said mass spectrometric method uses ESI-TOF MS.

32. (Currently Amended) A method for sequencing the terminal portion of an oligomer, comprising:

(a) contacting a first sample of said oligomer with a labeling moiety to covalently attach a label to the terminus of the oligomer and form a labeled oligomer, said labeling moiety having one element with an atomic number from 17 to 77, with the proviso that said element is other than sulfur or phosphorus;

(b) contacting a second sample of said oligomer with a labeling moiety to covalently attach a label to the terminus of the oligomer and form a labeled oligomer, said labeling moiety having two elements with an atomic number from 17 to 77, with the proviso that said elements are other than sulfur or phosphorus;

(c) optionally, repeating step (b) from one to three times with additional samples, wherein the labeling moieties have three, four or five elements,

respectively, with an atomic number from 17 to 77, with the proviso that said elements are other than sulfur or phosphorus;

(d) mixing the labeled oligomers from steps (a) through (c);

(e) fragmenting said labeled oligomers using an enzymatic, chemolytic or mass spectrometric fragmentation method to produce labeled oligomer fragments; and

(f) ~~analyzing said labeled oligomer fragments using a mass spectrometric fragmentation method to determine~~ **determining** the sequence of at least two terminal residues **of said labeled oligomer fragments, said sequence determination step comprising identifying a mass spectrum data corresponding to said labeled oligomer fragment or a mass spectrum fragment thereof, wherein said identification step is based at least in part on the mass defect of at least a portion of said labeling moiety.**

33. (Original) The method of claim 32, wherein each of said elements has an atomic number of from 35 to 63.

34. (Original) The method of claim 32, wherein each of said elements has an atomic number of from 39 to 58.

35. (Original) The method of claim 32, wherein each of said elements is selected from the group consisting of bromine, iodine, europium and yttrium and said oligomer is a protein.

36. (Original) The method of claim 32, wherein each of said elements is selected from the group consisting of bromine, iodine, europium and yttrium and said oligomer is an oligonucleotide.

37. (Original) The method of claim 32, wherein each of said elements is selected from the group consisting of bromine, iodine, europium and yttrium and said oligomer is an oligosaccharide.

38. (Currently Amended) A method for sequencing a portion of an oligomer, comprising:

(a) fragmenting aliquots of said oligomer using one or more specific enzymatic or chemolytic fragmentation methods to produce oligomer fragments, wherein a different fragmentation method is applied to each aliquot;

(b) contacting a first aliquot of oligomer fragments with a first labeling moiety to covalently attach said first labeling moiety to the terminus of the oligomer fragments and form labeled oligomer fragments, said first labeling moiety having one element with an atomic number from 17 to 77, with the proviso that said element is other than sulfur or phosphorus;

(c) optionally contacting the other aliquots of oligomer fragments with other distinct labeling moieties to covalently attach said distinct labeling moieties to the termini of the oligomer fragments and form labeled oligomer fragments, said distinct labeling moiety having two or more elements with an atomic number from 17 to 77, with the proviso that said elements are other than sulfur or phosphorus;

(d) optionally mixing the aliquots of labeled oligomer fragments; and

(e) ~~analyzing said labeled oligomer fragments using a mass spectrometric fragmentation method to determine~~ **determining** the sequence of at least two residues of said **labeled** oligomer, **said sequence determining step comprising identifying a mass spectrum data corresponding to said labeled oligomer or a mass spectrum fragment thereof, wherein said identification step is based at least in part on the mass defect of at least a portion of said labeling moiety.**

39. (Original) A method in accordance with claim 38, wherein said oligomer is a lipid.

40. (Original) A method in accordance with claim 38, wherein said oligomer is a protein.

41. (Original) A method in accordance with claim 38, wherein said oligomer is a nucleic acid.

42. (Original) A method in accordance with claim 38, wherein said oligomer is an oligosaccharide.

43. (Original) A method in accordance with claim 38, wherein said elements have an atomic number of from 35 to 63.

44. (Original) A method in accordance with claim 43, wherein said elements have an atomic number of from 39 to 58.

45. (Currently Amended) A method for comparing the relative abundances of analytes from two or more samples, comprising:

(a) contacting the analytes of the first sample ~~with~~ with a labeling moiety to covalently attach a label to the analytes and form labeled analytes, said labeling moiety having one element with an atomic number from 17 to 77, with the proviso that said element is other than sulfur or phosphorus;

(b) contacting the analytes of subsequent samples with labeling moieties to covalently attach labels to the analytes in each sample, wherein the labeling moieties used for each subsequent sample contain an additional element with an atomic number from 17 to 77, with the proviso that said elements are other than sulfur or phosphorus;

(c) mixing the aliquots of labeled analytes; and

(d) analyzing said labeled analytes using a mass spectrometric fragmentation method to determine the relative abundances of one or more of the analytes between the samples, **said analysis step comprising identifying mass spectrum data corresponding to said labeled analytes or a mass spectrum fragment thereof, wherein said identification step is based at least in part on the mass defect of at least a portion of said labeling moiety.**

46. (Original) A method in accordance with claim 45, wherein said elements have an atomic number of from 35 to 63.

47. (Original) A method in accordance with claim 45, wherein said elements have an atomic number of from 39 to 58.

48. (Currently Amended) A method for tagging the elements of chemical libraries, either during synthesis or screening, comprising;

(a) contacting a root tag with a labeling moiety to covalently attach a label to the root tag and form a labeled tag, said labeling moiety having one element with an atomic number from 17 to 77, with the proviso that said element is other than sulfur or phosphorus;

(b) optionally, contacting a root with additional labeling moieties to covalently attach additional labels to the root tag and form a multiply labeled tag, said labeling moiety having one element with an atomic number from 17 to 77, with the proviso that said element is other than sulfur or phosphorus; and

(c) analyzing the labeled tag by mass spectrometric methods to determine both its mass and the number of elements with an atomic number from 17 to 77, such that the mass and number of elements identifies the chemical processes to which the specific chemical of the library has been exposed and the identity of the chemical from the library, **said analysis step comprising identifying mass spectrum data corresponding to said labeled tag or a mass spectrum fragment thereof, wherein said identification step is based at least in part on the mass defect of at least a portion of said labeling moiety.**

49. (Original) A method in accordance with claim 48, wherein said elements have an atomic number of from 35 to 63.

50. (Original) A method in accordance with claim 48, wherein said elements have an atomic number of from 39 to 58.

51. (New) The method of claim 1, wherein said sequence determination step comprises identifying a mass spectrum peak of a fragment comprising said labeling moiety based on the mass defect of said labeling moiety.

52. (New) The method of claim 45, wherein at least a portion of said labeling moiety of step (a) is a stable isotope of said labeling moiety of step (b).

53. (New) The method of claim 52, wherein said labeling moiety of step (a) and said labeling moiety of step (b) differ by 2 or more but 16 or less stable isotopes.

54. (New) The method of claim 52, wherein said labeling moiety of step (a) and said labeling moiety of step (b) differ by 4 or more but 16 or less stable isotopes.

55. (New) The method of claim 52, wherein said labeling moiety of step (a) and said labeling moiety of step (b) differ by 8 or more but 16 or less stable isotopes.

56. (New) The method of claim 52, wherein said stable isotope is selected from the group consisting of ^2H , ^{13}C , ^{15}N and ^{81}Br .

57. (New) The method of claim 45, further comprising separating at least a portion of said mixture of labeled analytes prior to said analysis step (d).

58. (New) The method of claim 57, wherein said separation step comprises separating at least a portion of said mixture of labeled analytes by electrophoresis, chromatography or affinity separation.